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SequenceName : SEQ ID 476
5 SequenceDescription :

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<213> OrganismName : Helicobacter pylori, strain J99

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2235

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<212> Type : DNA <211> Length : 3714

SequenceName : SEQ ID 479 SequenceDescription :

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                                                                            900
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ctcagcgagc aagattacaa aataaaccgc ttcgctaatt tgcgcccctt aaaccaaaaa
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     gtgggcggga ctttcagctt cacttactac gggcagttga tgactaggga ctttcaggtg
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     agetetaget acaatagege taacatggtt acttgtttta gegaagegge atgeagggeg
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     tgggcggagg tagaaaaccc tgtgcgttcc attaacaacg cttttgagcc taaagtgaat
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     ctgatcgtca ataccgggaa agtcaqqcaa acctttatca tgggtttgcg tttcatqacc
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     accacttttt tacaacgcca atacttaaac accaatgaat gcgccactaa aacgagcggt
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     aagcatggcg tttatagaaa ctggaataac tggcgcaaca attacacagc ggtctatttg
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     tttgtgcaat acaacaacga aaatgcgtct aactggatgc aaatccctga gaaggattta
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     ttagacgttt tgagctatgg aggagcggag tattttaccc aacactttga cacggtggaa
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     gcaggagcgc gctacaccta taaagataaa ttcagcttca atgcggacta ctttaggatt
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     tgggcgcgcg attttgccac cgggcagtat tcagtctata cgagcgggcc catgaaaggt
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     aatgtgcgcc ccattaatgg ctattctcaa ggcgtggagc tggaattgta ttacaggccc
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     attagagggt tgcaattcca tgccgctttc aactacattg acactcgtgt aactagccat
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     ggccctttaa ccgacttgaa cggggatgtg ctaaaaggga ctagctataa caagcatttc
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     ccttttgtaa gccctttcca attcattttt gacgctcgct acaattggcg taaaaccacc
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     attggtattt ctagctattt ttatagccgt gcttatagcg ggattagcaa cagcgcagca
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     ggaggctatt atgggatgca atactatagt ggggggaaca actatgaaag cgttcttaat
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     agoggttatc aatgogaagc ttggtgtatg acccaacatg aagggctctt gccttggtat
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     tgggtgtgga atatccaagt gagccaaatt ttctgggaaa acggaagaca cagagttaca
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     ggaagcttac aaatcaataa catcttcaac atgaagtatt attttacagg gattggctct
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     ttctaa
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     <211> Length : 2526
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           SequenceDescription :
     Sequence.
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     <400> PreSequenceString :
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     ggctttttta tcagcgcggg ctatcaaatc ggtgaagccg ctcaaatggt gaaaaacacc
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     ggcgaattga aaaaactttc agacacttat gagaatttga gcaacctttt aaccaatttt
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     aacaacctca atcaggcggt aacgaacgcg agcagccctt cagaaatcaa tgctgcgatc
                                                                             240
     gataatttaa aagcaaacac gcaagggcta attggcgaaa aaaccaattc cccggcgtat
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     caageggtgt atttggeget caatgeggeg gtagggetgt ggaatgteat egeetataat
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     gtccaatgcg gtcctggtaa cagtggacaa caaagcgtaa cctttgaggg ccaaccagga
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45
     cataattcaa gttccattaa ttgcaattta accggttata acaacggggt tagcggcct
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     ttatccattg agaattttaa aaagcttaat caggcttatc aaactatcca acaagcttta
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     aaacaagata gcggatttcc tgttttggat agtgcaggaa aacaagtaac tataacaata
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     acaacgcaaa ctaatggagc taataaaagt gaaactacta ctactactac tactactaat
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     gacgetcaaa ceettttgea agaagecagt aaaatgataa gegteetcae tacaaactge
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     ccatgggtca atcacaatca aggacaaaac gggggcgcgc cgtggggttt agatacggca
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     gggaatgtgt gtcaggtttt tgccacggaa tttagcgccg ttactagcat gatcaaaaac
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     gcccaagaaa tcgtaacgca agctcaaagc cttaaccagc aaaacaatca aaacgcgccg
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     caagatttca atcettacac ctctgctgat agggetttcg ctcaaaacat gctcaatcac
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     gegeaagege aagecaagat acttgageta geegateaaa tqaaaaaaga cettaacact
                                                                            1020
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     atcccaagcc aatttatcac aaattacttg gcagcttgcc acaatggggg tgggacatta
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     cctgatgcgg gggttactaa caacacttgg ggggccggtt gcgcgtatgt ggaagagacg
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     ataacggctt taaacaacag ccttgcgcat tttggcactc aagctgagca aatcaagcaa tctgagttgt tggcgcgcac catacttgat tttagaggca gccttagtaa tttaaacaac
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                                                                            1260
     acttataaca gcatcaccac gaccgcttca aacacgccta attccccatt ccttaaaaat
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     ttgataagcc aatccactaa ccctaataac cccgggggct tacaggccgt ttatcaagtc
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     aaccaaagcg cttattcgca attattaagc gccacgcaag aattagggca taaccctttc
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     agacgcgttg gattaatcag ctctcaaacc aacaatggtg ccatgaatgg gatcggtgtg
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     caagtgggct acaaacaatt ttttggtgaa aagagaaggt gggggttaag gtattacggc
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     ttttttgact ataaccatgc ttatatcaaa tctagctttt tcaattcggc ttctgatgtg
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     ttcacttatg gggtagggac agatgtcctc tataacttta tcaatgataa aaccaccaaa
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     aacagcaaga tttcttttgg ggtgtttggg gggattgcgt tagctggcac ttcatggctg
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     aattcccagt atgtgaattt agcgaccttc aataatttct atagcgctaa aatgaatgtg
                                                                            1800
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gcgaatttcc aattcttgtt caatttaggc ttgagaatga acctcgctaa gaataagaaa
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     aaagcgagcg atcatgcggc tcagcatggc gtggaattag gcgtgaagat ccccacgatc
                                                                            1920
     aacacgaatt actattettt getaggeact caactecaat accgaagatt gtatagegtg
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     tatttgaatt atgtgttcgc ttactaa
                                                                            2007
     <212> Type : DNA
     <211> Length : 2007
           SequenceName : SEQ ID 487
           SequenceDescription :
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     ggctttttca tagaagccgg ctttgaaact gggctattag aaggcacaca aacgcaagaa
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     aaaagacaca ccaccacaaa aaacacttac gcaacttaca attatttacc cacagacacg
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     attttaaaaa gagcggctaa tttattcacc aatgccgaag cgatttcaaa attaaaattc
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     tcatctttat cccctgttag agtgttgtat atgtataatg gtcaattaac tatagaaaac
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     ttcttgcctt ataatttaaa taatgttaag cttagtttta cagacgctca aggcaacacg
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     attgatctag gcgtgataga gaccatcccc aaacactcta agattgtttt acccggggag
                                                                             420
     gcgtttgata gtttaaaaga ggcgtttgat aaaattgacc cctatacttt atttcttcca
                                                                             480
     aaatttgaag ccactagcac ttctatttct gatactaaca cgcagagggt gtttgaaacg
                                                                             540
     ctcaataaca ttaaaacaaa tcttataatg aaatatagta atgaaaatcc aaacaatttc
                                                                             600
     aacacttgtc cttacaataa taatggtaat acaaaaaatg attgttggca aaatttcacc
                                                                             660
25
     ccacaaaccg cagaagaatt caccaattta atgttgaaca tgatcgctgt cttagactcc
                                                                             720
     caatcttggg gcgatgcgat cttaaacgct ccttttgaat tcactaacag ctcaacagat
                                                                             780
     tgcgatagcg atccttcaaa atgcgtaaat cccggagtaa atgggcgtgt tgatactaaa
                                                                             840
     gtcgatcaac aatatatact caacaaacaa ggtattatta ataattttag aaaaaaaata
                                                                             900
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     gaaattgatg cggttgtttt aaaaaattca ggggttgtag ggttagccaa tggatatggc
30
     aatqatqqtq aatatqqcac attaqqqqta qaaqcctatq ctttaqatcc taaaaaactc
                                                                            1020
     tttggcaacg accttaagac tatcaattta gaagatttaa gaaccatctt gcatgaattc
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     agccacacta aaggctatgg gcataacggg aatatgacct atcaaagagt gccggtaacg
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     aaagatggtc aagtggaaaa ggatagtaat ggcaagccaa aagattctga tggcctcccc
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     tataatgtgt gttcgcttta tgggggatcc aatcagcccg ctttccctag caactaccct
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     aattccatct atcacaattg tgcggatgtc ccggctggct ttttaggggt aacagcagcg
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     caaacaaact acaacctaaa cgctagttta aacacgcaag atttagccaa ttccatgctc
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     agcaccatcc aaaaaacctt tgtaacttct agcgttacca accaccattt ttcaaacgca
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     tegeaaagtt ttagaageee tattttaggg gttaaegeta aaataggeta teaaaaetae
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     atcaccactt actccaataa aaatagccct acaggcattc aaaccaaaag gaatttttct
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                                                                            1800
     aaagtcaaag gaagcggcaa tttagatgtg gctaccgggt tgaactaccg ctataagcat tctaaatatt ctgtagggat tagcatccct ttaatccaaa gaaaagctag cgtcgtttct
                                                                            1860
45
                                                                            1920
     agcggtggcg attatacgaa ctcttttgtt ttcaatgaag gggctagcca ctttaaggtg
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     tttttcaatt acgggtgggt gttttag
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           SequenceDescription :
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                                                                             120
     tatttagggg ttgggtatca gcttagcgcg atcaacacgt cttttagcac cagttctata
                                                                              180
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     gataaatcgt atttcatgac cggcaatggt ttttggcgtgg tgttgggggg gaaattttgtg
                                                                              240
     gctaaaacgc aagctgtaga gcatgtgggt tttcgttacg ggttgtttta tgatcagacc
                                                                              300
     ttttcttctc acaaatccta tatttctacc tatggtttag aatttagcgg tttgtgggac
                                                                             360
     getttcaatt egecaaagat gtttttgggg ttggagtttg gettaggeat egetggggeg
                                                                              420
                                                                              480
     acttacatgc caggagggc catgcatggg attatcgctc aatatttagg caaagaaaat
65
     tcgcttttcc aattgcttgt gaaagtgggt tttcgttttg gctttttcca caatgaaatc
                                                                              540
     acctttgggt tgaaattccc tgtcattcct aacaaaaaa cggaaatcgt tgatggcttg
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     agegegacea etttatggea aegettgeeg gtageetatt teaattatat etataatttt
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tag
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     gctgaagaca acggcgtttt tttaagcgtg ggctatcaaa tcggtgaagc ggttcaaaag
                                                                            120
     gtgaaaaacg ccgacaaggt acaaaagctt tcagacgttt atgaacaatt aagcaagctt
                                                                            180
     ttagccaacg ataatggcac tagctcaaaa acaagcgcgc aagcgatcaa_tcaagcggtt
                                                                            240
15
     aataatttga atgaaagcgc aaaaacttta gccggtggga caaccaattc ccctgcctat
                                                                            300
     caagecaege ttttageatt qagateggeg ttagggttat ggaatageat gggetatgeg
                                                                            360
     gtcgtatgcg gaggttatat taaaaaaccg ggcgaaaaca atcaaaaaaa tttccactac
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     accgatgaga atggcaacgg cactacaatc aattgcggtg ggagcacaaa tagtaatggc
                                                                            480
     actcatagtc ctaatggcac aaatacatta aaagcagaca aaaatgtttc tctatctatt
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     gagcaatatg aaaaaatcca tgaagcctat caaatccttt caaaggcttt aaaacaagct
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     gggcttgctc ctttaaatag caaaggggaa aagttagaag cgcatgtaac cacatcaaag
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     gatcaacaag gaacatccag tgaccaaact acaaccacaa cttctgttat tgatacgact
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     aatgatgege aaaatetttt gacteaageg caaacgattg teaataceet taaagattat
                                                                            780
     tgccccatgt tgatagcgaa atctagtagt aatggtggaa ctaatggcgc aaacacccct
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     tcatggcaaa cagccggtgg cggcaaaaat tcatgtgcga cttttggtgc ggagtttagt
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     gctatttcag acatgattag taacgctcaa aaaatcgttc aagaaaccca acaacttaac
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     gccaaccaac ccaaaaatat caccaaccc aataatttca accttaactc tcctggcagt
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     cttacggctt tagctcaaag catgctcaaa aacgctcaat ctcaaacaga aattttaaaa
                                                                           1080
     ttagccaatc aggtagcaag cgattttgac aaactttctt caggctatct taaagattac
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     atagggaaat gcgatgtgag tggtgtgagt agttcaaata tgacaccgca aaatatgaat
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     accacttggg ggaaaggctg cgcgggcgtg gaagaaactc taacttcgtt aaaagcaagc
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     accactgatt ttaacaacca gacaacgccc caactcgatc aagcgcaaac cctagccaat
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     accettacte aagaactegg caataaceet tteaaacgag tgggtateat tggeteteaa
                                                                           1380
     accaataacg gggcgatgaa tggccttggg gtgcaagcgg gttataagca attctttggt
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     caaaaaagaa ggtggggtt aaggtattac ggcttttttg actacaacca tacctacatc
     aaatccagct tttttaactc gtcttctgac gttttgactt atggggtggg tagcgattta
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     ttgtttaatt tcatcaatga taaaaacacc aatttcttag gcaagaacaa taagatttct
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     aatttaaaaa ccatcagcaa tgtttatagc gctaaagtga atacggctaa tttccaattc
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40
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     ttattcaatt taggcttgag aaccaatctc gctaggccta agaaaaaaga cagcgatcat
     tccgcgcaac atggcatgga attgggcgtg aaaatcccta ccattaacac gaattactat
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     tottacttgg gaactaaact agaataccga agactctata gcgtgtatct caattatgtg
                                                                           1920
     tttgcgtatt ga
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     gtttatatga gcgtgggcta tcaaatcggc gaagccgcac aaatggtgaa aaacaccggc
                                                                            120
55
     gaaatccaaa aagtctccaa cgcttacgaa aatttgaaca accttttaac ccgctataat
                                                                            180
     gaactcaaac aaacggcctc taacactgat tcaagcaccg ctcaagcgat tgacaatcta
                                                                            240
                                                                            300
     gaaaagagcg ctagcagatt gaaaacgacc cctaataccg ccaatcaagc cgtgtcctca
     gegeteaget etgeggtggg catgtggcaa gtgatageet etaatttage caacaacteg
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     ctatetteta gegaataega aaaaeteaaa gegaettete aattgeteea aaataeeeta
                                                                            420
60
     gaaaataaaa acaataatct taaaattgaa aatgactatg accagctttt aactcaagct
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     agtaccatta ttaataccct tcaaagccaa tgcccaggcg tagatggggg caatggcaaa
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     ccatggggca ttaatacaag cgggaacgca tgcgctattt ttggtagcac ctttaacgcc
     attaatagca tgattgatag cgctaaaaaa gccgccgcag atgcccgaag aactgcccca
                                                                            660
     gaaagtccaa accaacaaaa cgcgtttacc aacgctgatt tcaataaaaa cctcaatcaa
                                                                            720
65
     gtctcaagcg ttatcaatga caccatctct tacctcaaag gggacaattt agaaaccatc
                                                                            780
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     tacaacacca ttcaaaaaac gcctaattct aaagggtttc aaagtttggt gagccggtct
     agctatagtt attototoaa ogaaacccaa tattotoaat tooaaactac caccaaagag
                                                                            900
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960
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     gggatccggt attatggctt ttttgattac aactatqcqt atatcaaatc caattttttc
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     aactccgctt ccaatgtttt cacctatggc gcgggcagtg atcttttatt gaacttcatc
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     aatggcggat ccgatcgaaa ccgcaaagtc tcttttqqca ttttttggggg catcgctcta
                                                                          1200
     gcgggaacga catggcttaa taaccaatct gcgaatttaa aaatcaccaa tagcgcctac
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     agegetaaga teaacaacae caattteeaa ttettgttea ataceggttt aaggetteaa
     gggatccatc atggcattga attaggcgtg aaaatcccta cgatcaacac caattactat
                                                                          1380
     tettteatgg gegetaaatt agectaeege aggetttata gettgtaeet eaattatgtt
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     ttggcttatt ga
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     <212> Type : DNA
     <211> Length : 1452
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         ~ SequenceDescription :
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     Sequence
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     <400> PreSequenceString :
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     tttgaagcta agctcaacgg ctttgtggat caatccagca cgatcggttt taaccagcat
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     aaaatcaata aagaaagagg catctaccct atgcagcaat tcgcaacgat tgcgggctat
     ttagggcttg gttttagcct gttacccaaa aaggtttcag accatgttct aaaaggcaaa
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     atagggggca tggtcggatc tattttctat gacggcacga agaagtttga agacggctct
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25
     gtggcttaca acctctttgg ttattacgat gggtttatgg gggtctatac taatatctta
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     caaaccgata gccttgagac acagaacatg aaacacaaca aaaatgtccg caattatgtc
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     tttagcgacg cgtatttaga atacgcttat aagaattatt ttgaaataaa agccgggcgc
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     tttttaatgg attggtttgc cgcacggacc acttatagcg gaggctttac caaaaacaat
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     aatggaggtt atgatagcca tgggcgaaag gtgctttatg gcacgcatgc ggtgcaactc
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     acctataaac ctcatcgttt cctcatagaa ggcttttatt acctttcgcc tcaaatcttt
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     aacgetecag gegttaagat tggttgggae tetaaceeta attttagegg cacaggettt
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     cgctctgata cggctatcat agggtttttc cccatttact acccttggat gatcgttaaa
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                                                                            960
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     tttcaaaacg ctaatggttg gataggcaac atggggaatc caagcggtgt gatcatgggg
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     aqtaacaqcq totatqcaqq ttttacaqqc acaqccctta aaagagacgc cgctaccatt
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     aaaaacaccg gcgaattgaa aaacttgaac gacaaatacg agcagttaag ccaatcttta
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     cttcaaaccg cgcaacagct catggactta atcgaacaga ccaaggtttc tatggtgtgg
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     caaaagcaaa teetttetaa egetteaagt atetteaate tetttaatte catteetaaa
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     ctaaaatcca atcaaacaga gatcgtaacc acttataacg atgctaagaa tttgagcgaa
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     <211> Length : 1917
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           SequenceDescription:
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     ttctccaaag tgggttttaa ccgttcgcct attaaccctg ttaaaggtat ctatcctaca
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     accetgaate taggoggtet tttgggogga caagtttate ataacactae gtatgatage
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     cctacaaaga atctaatgat ccacccttat gtgtatctca tcccaatggt aggtacattg
     cccggtgcta aaatagaata cgataccaat cctgagttta gcggtagagg tataaggaat
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     gcacccqctc gttataacac ttgggatccg ttcttggata atggtaagtg gcgtggcttg
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     aagcatggta agttcagttg gagcgtttat cagcgcttca ctaccgcacc aagggctttg
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     aaactcgtgt ggttagagtt ccaaatccgt gcgggttaca accctggaac cggtttcctt
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     gggccaaacg gtcagccgct caacttgaat aatggtttgt ttgaatcttc ggcgttcgcg
                                                                             1500
     caaggccctc aaaacatggg tggtatcgca aaaagcatta ctcaagacag aagccatttg
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     <211> Length: 1587
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SequenceName : SEQ ID 501

SequenceDescription :

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Sequence
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                                                                          120
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    qqcacqqctt taqqctcqqc qtatqtcqct qqqgctaggg gtgctgacgc ttctttttac
    aacccggcta acatgggctt tactaacgat tggggcgaaa acagaagcga atttgaaatg
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    aacactatag ggttaggcaa tatccttaaa gcgcttggca atacggccgc taccaatggc
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  ttatcacaaq ctatcaatcq tgttcaaggg cttatgaact taaccaatca aaaagtcgta-
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    accetegett caaaacetga cacteaaate gtgaatgget ggacaggeac gactaatttt
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    gacgtgttta tcatgatggt agagcttgcc cctagcatga gttatactat taataaacgc
                                                                          720
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    ttttacaacg gcttgaaaaa aatcatgggt tatagcggtt taatcaaagc gagcgcgaat
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    ttagcctacg cccaccaatt ttttaaagat cgcctaaggg ttgaaggggt gtttgagcgc
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    actitttgga gtcaagggaa taaattitta gtcacccctg attttgcgaa cgccacttac
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    tttqqqacta aatacaattt taggggcttt gatttgggcg tagcggggag tttcactttt
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          SequenceDescription :
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     actcaaaacg cacttaaaac ttcattggag cgattgagtt caggtttaag gatcaataaa
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     geggetgatg acgeateagg catgaeggtg geggattett tgegttegea agegageagt
     ttgggtcaag cgattgccaa cacgaatgac ggcatgggga ttatccaggt tgcggataag
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     ateggeteta ecaetteega taaaateggt caggttegta tegetacagg egegttaate
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     ttaggettea eggegattgg ttttggggaa teteaagtgg eagaaaceae ggtgaatttg
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     gccgtgatcg ctagcggtaa ccaaagcttg ggatctgggg ttacaacctt aagaggcgcg
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    ttcaacaaaa acaacatttt ggcgcaatca ggcagctatg cgatgagtca agccaatacc
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    aatcctagcg ctattgaagc ttatgcgacg aatcaaatcg ctgttcctag cgtgccaaca
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    acqqttqaaa tqatqaqcqq tatattaqqc aatattacaa gcgcagcacc aaaatacgcc
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     ctagetetae aagageaact gegtteteaa geaageaaca geteaatgaa tgatacagee
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     aacataaget egetatataa ttacaatata gtagegaata aatettttt gaaategeat
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     <211> Length : 1113
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65 Sequence

<213> OrganismName : Mycobacterium tuberculosis H37Rv

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### WO 2005/076010 PCT/IN2005/000037 218/341

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#### Sequence

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# WO 2005/076010 PCT/IN2005/000037 230/341

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						ttgccaaggc	
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65				arggrrgrcg	Etgacggcaa	gtcttacgta	5100 . 5121
65		ctatcaagta	a				7777
	<212> Type						
	<211> Lengt	لد کبلار ، بیب					

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SequenceName : SEQ ID 559 SequenceDescription :

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Sequence
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     <400> PreSequenceString :
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     ctaagtgaag ccgatgtgga gtgtacaatc aaaatagaag ccgaggatgg ctatgccaac
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     gacatttggg cagaceteaa eggaaaegge aagtaegatt egggggagag getegattea
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     ggtgagtttc gtgatgttga gttcagacaa acaaaqqcca tcgtctatgg caaaatqqcc
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     aaattottgt ttagaggtto ttotgcaggg gactatggtg ctacctttat agatattago
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     aattgtaccg geetgactge tttcgactge tttgccaatc tgctgacaga actcgatetg
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     tccaaagcaa acggtctgac ttttgtaaac tgcggcaaaa accagctgac caagcttgac
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     ctgcccgcaa atgcggacat tgagacgctg aactgctcca aaaacaagat aacgagtctc
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     aacctatega cetataceaa getgaaagag etttatgtgg gegacaaegg getgaeagee
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     ttggatctct ccgccaatac gctcctcgaa gagctggtgt attctaacaa cgaggtgact
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     acgataaacc tgtctgccaa tacgaacttg aaaagcctgt attgcataaa caataagatg
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20
     accggactcg atgtcgcagc caacaaagag ctgaaaatac tccactgcaa caacaatcag
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     ctgaccgccc tcaatctctc ggccaatacc aagctgacga ctctaagctt cttcaacaac
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     aacaaccagc tgactgctct ggatctgtca aaaacgccga aactgacaac gttgaattgc
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25
     tactccaacc ggatcaaaga taccgccatg cgtgcattga tcgaaagcct gcctacgatc
                                                                           1080
     actgaaggag aaggcaggtt cgttccttac aacgacgatg aaggaggaga agaggagaac
                                                                           1140
     gtgtgtacaa ccgaacacgt ggaaatggcc aaggccaaga attggaaggt acttacctcg
                                                                           1200
     tggggagagc ctttccccgg aataacggct ttgatttcca tcgaaggtga gagcgaatat
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     teegtatatg eteaagatgg cateetetae eteteeggta tggageaggg ettgeeegtt
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30
     caggitatata cogtgggagg aagcatgatg tactcatctg togcitcogg atcagcoatg
                                                                           1380
     gaaatacago tocogagagg tgcagootat gtagtacgta toggcagooa tgcgatcaaa
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     <211> Length: 1455
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           SequenceDescription:
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40
     <213> OrganismName : Shigella flexneri 2a str. 2457T
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     tcattcgcct gtaaaaccgc caatggtacc gctatcccta ttggcggtgg cagcgctaat
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     gtttatgtaa accttgcgcc tgtcgtgaat gtggggcaaa acctggtcgt agatetttcg
                                                                            180
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     acgcaaatct tttgccataa cgattatccg gaaaccatta cagactatgt cacactgcaa
                                                                            240
     cgaggetegg ettaeggegg egtgttatet aattttteeg ggaeegtaaa atatagtgge
                                                                            300
     agtagctatc catttccgac caccagcgaa acgccgcggg ttgtttataa ttcgagaacg
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     gataagccgt ggccggtggc gctttatttg acgcctgtga gcagtgcggg cggggtggct
                                                                            420
     attaaagctg gttcattaat tgccgtgctt attttgcgac agaccaacaa ctataacagc
                                                                            480
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     gatgattttc agtttgtgtg gaatatttac gccaataatg atgtggtggt gcccactggc
                                                                            540
     ggttgtgatg tttctgctcg tgatgtcacc gttactctgc cggactaccc tggttcagtg
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     ccaattcctc ttaccgttta ttgtgcgaaa agccaaaacc tggggtatta cctctccggc
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     acaaccgcag atgcgggcaa ctcgattttc accaataccg cgtcgttttc accagcgcag
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     ggcgtcggcg tacagttgac gcgcaacggt acgattattc cagcgaataa cacggtatcg
                                                                            780
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     ttaggagcag taggaacttc ggcggtaagt ctgggattaa cggcaaatta cgcacgtacc
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           SequenceDescription :
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	cgttcgccct	caattcaact	gataaaattt	ggcgctattg	gtttgaatgc	aattatcttt	120
	tacacactga	tgatagctgc	tgatacagga	agtcaatatg	gcaccaatat	tactattaat	180
					gaaacctcta		240
_					atgatgtcac		300
5					gcaaaaaacag		360
					ccatcggcat ttaagagtaa		420 480
					tcaccattga		540
					atcttggaag		600
10					tcaacggcaa		660
					ttcagggcta		720
					caaacagtac		780
					ttagcgcgaa		840
1.5						aaccactatc	
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					tgcaaæatac		1080 1140
					tcageggcgg ggatttatgc		1200
20					gtaca cccga		1260
					tcaacgcctc		1320
					atctggatat		1380
					gcgggaaact		1440
					tcgacacgct		1500
25					gcaca tttac		1560
					ctgatgttgt		1620
					ggagt agtgc		1680
					gaaat gaagt		1740
30					ctcaggttga		1800
50					tttacgette ctcag cetce		1860 1920
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	ggcaattatc	tcaatqtcqq	ttacttattq	aactatgttg	aaaac cgtac	gctgatgcaa	2040
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35					ttgacatggg		2160
					cgttg tatgt		2220
	attgactcaa	cacatgcatc	gccggactat	agcggaggcg	acggt accgc	acgttcagac	2280
					tttac agcga		2340
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40					ccggg cagag		2460
					agctt acata		2520
					atctgaatca ccgcaggcaa		2580 2640
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					cggat tacac		2820
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	Seque	enceDescript	cion :				
	_						
	Sequence						
55	42125 0	nismName : S	Thimalla El		04 E7M		
55	_	guenceStri	_	exileri za si	Cr. 245/1		
				acaacaataa	tgatgggcgt	atteacetet	60
					tttacggcac		120
					ttgat atggg		180
60					gtttc cagat		240
					ttact ggtac		300
					ccggt gcggc		360
	gttagcctgg	cgatcggtga	ctctctgggt	acctcttaca	aaagc ggcat	gggtattgac	420
	cagaaaatag	tgaaagacac	ttctaccaac	aaaggcaaag	cgaag cagac	actgaacttt	480
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	_	ttacttacct	gtaa				564
	<212> Type	: DNA					

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<211> Length : 564
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           SequenceDescription:
 5
     Sequence
     <213> OrganismName : Shigella flexneri 2a str. 2457T
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     gctctggccg atactacgac ggtaaatggt gggaccattc actttaaagg ggaagttgtt
                                                                            120
     aacgccgctt gcgcagttga tgcaggctct gttgatcaaa ccgttcagtt gggacaggtt
                                                                            180
     cgtaccgcta gcctgaagca ggctggagca accagctctg ccgttggttt taacattcag
                                                                            240
     ctgaatgatt gcgataccac tgttgccaca aaagccgctg ttgccttctt aggtacggca
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     attgatgcta cgcgtactga tgtactggct ctgcagagtt ctgctgcagg tagtgcaaca
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     aacgttggcg tgcagatcct agacagaaca ggcaatgctc tgacgctgga cggtgcgaca
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     tttagtgcac aaacaaccct gaataacggt accaacacca ttccgttcca ggcgcgttat
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     Sequence
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     agcctcaccg ccgcgcaaaa agcgacgcta acccctattt caaatcagca atcgtcgttt
                                                                            120
30
     acceptaaac ttagegeeta eggtaegetg aaaagegege tgaegaettt ccagaeegee
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     aatactgcat tgtctaaagc cgatctttt tccgccacca gcaccaccag cagcaccacc
                                                                           240
     gcgttcagtg ccaccaccgc gggtaacgcc atcgccggga aatacaccat cagcgtcacc
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     catctggcgc aggcgcaaac cctgaccacg cgcaccacca gagatgatac gaaaacggcg
                                                                            360
     ategecacca gegacageaa acteaceatt caacaaggeg aegacaaaga teegattace
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35
     attgatatca gegeggetaa eteategtta agegggatee gtgatgeeat caacaacgea
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     aaagcgggcg taagtgcgag catcattaac gtgggtaacg gtgaatatcg tctgtcagtc
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     acatcaaatg acaccggcct tgataatgcg atgacactct cggtcagcgg tgatgatgcg
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     ctacaaagtt ttatgggcta tgacgccagt gccagcagca acggtatgga ggtctcggtc
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     gccgcccaga atgcgcagct gacggtcaac aacgtcgcca tcgagaacag cagcaacact
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     atcagcgacg cgctggaaaa catcactctg aacctgaacg atgtcaccac gggcaaccag
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     acgctaacca tcactcagga cacctccaaa gtgcaaacgg cgattaaaga ctgggtgaat
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     gcctataact cgctaataga taccttcagc agcctgacca aatacaccgc cgtagatgcg
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     ggagctgata gccagagttc tagcaatggc gcactgctcg gcgactccac gctgcggacg
                                                                            960
     attcagacgc agttgaagtc gatgctgagt aataccgtca gttcttccag ctataaaacg
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     ctggcgcaga ttggtatcac gaccgatccc agcgatggca aactggaact ggatgccgac
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     aaactcaccg ctgcactgaa aaaagatgcc agcggcgtag gtgcattgat tgttggcgat
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     ggtaaaaaaa ccggcatcac aaccaccatc ggcagcaacc tgaccagttg gctttcgaca
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     acgggcatta ttaaagccgc taccgatggc gttagtaaaa ccctgaataa gttaactaaa
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     gactacaacg ccgccagcga tcgcattgat gcgcaggtcg cgcgctacaa agaacaattt
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     acceaactgg acgttttaat gacctcgtta aacagcacca gcagctactt aacgcagcag
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     <211> Length : 1407
           SequenceName : SEQ ID 565
53
           SequenceDescription :
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     <213> OrganismName : Shiqella flexneri 2a str. 2457T
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                                                                             60
     ggacacacag ccactaatac ccgcgtggat gatggcggaa cgctggatgt ccgcaacggt
                                                                            1.20
     ggcaccgcca ccaccgtatc catgggaaat ggcggtgtac tgctggccga ttccggtgcc
                                                                            180
     getgteagtg gtacceggag egacggaaag geatteagta teggaggegg teaggeggat
                                                                            240
65
     gccctgatgc tggaaaaagg cagttcattc acgctgaacg ccggtgatac ggccacggat
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     accacggtaa atggcggact gttcaccgcc aggggcggca cactggcggg caccaccacg
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     ctgaataacg gcgccatact taccetttcc gggaagacgg tgaacaacga taccetgacc
                                                                            420
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480
    atccgtgaag gcgatgcact cctgcaggga ggcgctctca ccggtaacgg cagcgtggaa
    aaatcaggaa gtggcacact cactgtcagc aacaccacac tcacccagaa agccgtcaac
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    cgcggtacag ccctgaagct gaccggcagc actgtgctga acggtgccat tgaccccacg
    aatgteacte tegectetgg tgccacetgg aatatteecg ataacgccae ggtgeagteg
                                                                           720
                                                                           780
    gtggtggatg acctcagcca tgccggacag attcatttca cctccacccg cacagggaag
                                                                           840
     ttcgtaccgg caaccctgaa agtgaaaaac ctgaacggac agaatggcac catcagcctg
     cgtgtacgcc cggatatggc acagaacaat gctgacagac tggtcattga cggtggcagg
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    accagoggta agggtattca ggtggtggaa gccattaacg gtgccaccac ggaggaaggg
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     gcctttatcc aggggaataa gctgcaggcc ggtgccttta actactccct caaccgggac
                                                                          1080
    agtgatgaga getggtatet gegeagtgaa aatgettate gtgcagaagt ceceetgtat
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     geotecatge tgacacagge aatggactat gaceggatte tggcaggete cegeagecat
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     ggtcacgata acaacggcgg tattgcccgt ggagccacgc cggaaagcag cggcagctat
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     gcgggggtat atggtgctgc tggccattct tccgttgatg ttaaggatga tgacggctcc
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     tcatcggaca ataacgactt ccgcgtccgg ggctggggct ggctgggttc gctggaaacc
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     agtgcacaac atgtgcgtgc cggcttccgt ctgggcagcc accacgatat gaactttggt
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                                                                          1860
     aaaggcacct catcccgtga caccctgcgc ggcagtgcca aacacagtgt gcgtgaactg
     ccggtgaact ggtgggtaca gccttctgtt atccgcacct tcagctcccg gggggacatg
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     agcatgggta cagccgcagc cggcagtaac atgacgttct caccgtcaca gaatggtacg
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     tcactggacc tgcaggccgg actggaagcc cgtgtccggg aaaatatcac cctgggcgtt
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     caggocagtt atgoccacag catcaacggc agcagogctg aaggttataa cagtcaggco
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     ggcaacaata tegecaacte egecacetae ggetttaaat eaggeaegge etettttgee
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     gatatgtttg ceggttegaa agtgggaetg ggggtaaaag ttgceggtat cacteaggae
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     tttaccgatg gcacgaccac caacaccggg cgaggtctgg acgttgctat cagccagaac
     ggttttttcc gtctggtaga cagcaacggt tcggtgttct acagccgtaa cggacaattt
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     aagctggatg aaaaccgtaa cctgttgaat acgcaaggtt tacagctgac gggttacccg
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     gtaaccggta cgccgccgac tattcagcaa ggggcgaatc cgaccaatat ttcgatcccg
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     aataccctga tggcagcgaa aactaccacc acggcgtcga tgcagatcaa cctgaattcc
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     agtgatccgc ttcctactgt tacgccattc agcgccagca atgcggatag ctataacaaa
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     aaaggttcgg tgactgtttt cgacagtcag ggtaatgctc atgacatgag cgtctatttt
     gtgaagaccg gggataataa ctggcaggtc tacacccagg atagcagtga tccaaacagc
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     agetteetea actecatgea geaaaatace ggegetaaca acattgtgge aaceaeceag
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     ggcaacaatt ccaacgaaca aacccaactg ctggggcaga ttgtactggc gaactttgcc
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     gtggcgctgt tggggacagc cgggacggga aactttggca ctctgaccaa cggtgcgctg
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     gaagcgtcca acgtcgatct cagtaaagaa ctggtcaata tgatcgttgc ccagcgtaac
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     tataagtota acgoccagao catcaaaaco caggaccaga tootcaacao gogggttaac
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<213> OrganismName : Shigella flexneri 2a str. 2457T

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     caacaacctg ctatccagca accgaatgtc tccggtactg tctggatccg tcagaaagtc
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     gcactgccgc ctgatgctgt gctgaccgtg acactttctg acgcgtcgtt agccgatgca
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     tttgttctgc catttaaccc ggcagatgtt cagccgaacg cgcgtattct gttqaqtqcq
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     gcgattaccg tgaatgacaa actggtattt atcaccgata ccgttcagcc ggtgatcaac
                                                                            420
     cagggeggaa ctaaagcega cetgacattg gtgceggtac agcaaacege cgtgceggtt
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     caggccagcg gtggcgcaac gactaccgta ccttcgactt caccaactca ggtgaatccg
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     tetteggeag tteeegetee tacgcaatat taa
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     <212> Type : DNA
     <211> Length : 573
       SequenceName : SEQ ID 568
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           SequenceDescription :
     Sequence
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     agtgcctttt ttctcaacac agcttacgcc tggcaacaag aatatatcgt tgatacgcaa
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     cooggacatt ccacagageg ttacacctgg gatagtgatc atcaacctga ttacaacgat
                                                                            180
     attttgtcgc aacgtattca aagtagccaa agggcgctgg gactggaagt caatctggcg
                                                                            240
25
     gaagaaactc ctgtggatgt gaccagcagt atgagtatgg gctggaattt tcctttatat
                                                                            300
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     ggcaatgaaa totattoggo taaggacaac caatataaag otaatggtgo aacotttaat
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     gettattatg gtgeaggtge tatgacttae aagggagaae cetteacett tactgttggt
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     ggtaatgatc aaaacttacc aacaaccatt tggtttgcga ctaattcagc tgtagctgtg
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     cctaaagatc cgggagctaa accaacaccg ccagaaaaac cagagttgaa aaaacctact
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     gtgacttggc ataaaaatct tgttgttgaa actaaaactg aggaagttcc tccagtgaca
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     ccaccaacaa ctcctgatga accaacgcca gaaaagccaa aaacaccaga ggatcctcaa
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     tcacctgtcg tagctaagtc agtaagcttt agaacggcaa gaaaaggaga aatgcgtgtt
                                                                           1620
     agagagcgtg attatcaacc gactetteca catgetgggg etgetaaaca aaatggttta
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           SequenceDescription :
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     ttaacgacta cagttgttgc ccttgcgtca ggtactgtaa tcgaggctga tgagacaata
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     gaacageetg tegeagetga gaetgteteg caagetgatg gggacaatee egaacaaaca
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     acaagcgttc aacaagaaac tgctcctcaa caaacgaaaa cttctcaaag ctcagacgca
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     accgtagata gtgaagagtc agcaacttcc ccatctgatg aacagaccgt aagtcaaaat
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     gattcaaact catcatctca aattgatcaa acgatagctg atacgaatcg ctctgactct
                                                                            360
65
     gatcatattt caaaaacatc agccgctaca actgaagatc aagaagagaa agttaattct
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540

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		ataatattgc					720
	gcacaagatc	gggctaacga	agaagccaat	gaaaaaaacg	gcttggatca	tgatactaat	780
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		ccaaaagtca					900
	tatctagcgc	ttaactggtt	ttctgactat	tttaatattt	acgatgaccc	caacgatggc	960
		ttggacacgc					1020
1.0		caggtcaaga					1080
10	_	acgaagataa	_				1140
		attataaagg					1200
	graaaaaaag	gcacttcccc	tgatgcagct	tctactcctc	acaacagtga	taaaccttca	1260
		ctaaagatct ctgttcatca					1320
15		accaaaattc					1380. 1440
13	aatcaattag	ccttgatagc	tttaggaaga	gggttgattt	tactttcccc	acttettett	1500
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	Sequence						
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		equenceStri	_				
		aaaagcaaaa					60
		tagctttctt					120
20		aaaggcaaac					180
30		aggtggaagc				_	240
		caactgatgc	_	_			300
		ctgttaatga cgcaaaacag					360 420
	_	ccccatcaca		_	-		480
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		attatgatag					660
		ggtattatct					720
		ctctgtattt					780
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		atggtgttaa					900
		ttgttaagac					960
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		tcaacagtta					1260
		gtcaaattat					1320
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50		ctattggcgg					1440
		ctgatattaa	_				1500
		aaagccattt					1560
		aaagttcaat					1620 1680
55		atgtagcaag gtggcggtat					1740
55		ctattgctgc					1800
	_	aagctctgaa	_		_		1860
		cagatagtag					1920
	caaaataaat	ggctttccta	ttatgaaact	aatottoota	aacatcactc	tagagtcact	1980
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		ccaagaattg					2100
		ctaaggctac					2160
		gaagaaggta				J	2181
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SequenceName : SEQ ID 600 SequenceDescription :

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     <213> OrganismName : Streptococcus mutans UA159
     <400> PreSequenceString :
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                                                                            120
     acaactattt tagctagtga tggttttcat caatatgtga tttttgatgc tctttttcgt
                                                                            180
     aatattetee atggaacgga tagtttgttt tactetttta aggetggget tggttttaat
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     atttttgctc tgacaagtta ttacttggga agttttttaa caccttttac ttacttttt
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     aatgtaaaaa atatggcaga tgctttttat ctcttcactt taatcaaatt tggtctaata
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     ggtttatctg ctttttacag tcttgggcaa atttatacta aaatctctaa atcactcgtt
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     ttgatgctgt caacatctta tgctttaatg agctttacta gcagtcagtt agaattaaac
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     aattggttag atgtttttat cotgotacca citattatgc ttggtttaca gcgtttagta
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     gaaaaaaggg ggatttttct ttattttcta actcttactt gtttatttat tcaaaattac
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     tattttggtt tcatgacage tattttctta actetttggt tttttacgca agtetegtgg
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     gatattagaa acagaatgaa acgattaagt gattttgtgc tcgtatcaat ctttgcaacg
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     ctgacaagtg cttttatgct gcttccaaca tttcttgatt taaagagcca tggtgaagta
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     ttaacagaac aaattagtet attttcatca gacatttggt atttcgattt ttttgctaaa
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     agtettettg gtagttatga tacgacaaaa tatggeteta ttecaacgat ttatateggt
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     ttacttccct tgatttttgc cattactttt ttctttgtta aatctataaa atggcaagtt
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     aaagtagett attttettt attggetatt attattgeaa gttttatett teaaceaett
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     gatttatttt ggcaaggaat gcattcacct aatatgtttt tgcatcgtta ttcttgggct
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     ttcaaggact attataatta tctgacacaa gttaatttta tattaacaac tatcttttta
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     gttagttatt ttattattet ttttactttt tttaatcaat tagtttetta taaaqttatt
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     atttccttta cacttatctt tacaagtttt gaaatagctt taaatacttt ttatcaaatt
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     gaaggtattc aaactgactg gaatttccct tcaagagagg tttatgaaga taatgtaaag
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     gaaattgaca actatgttaa gaaaactaaa aaagataact tagaattttt tcgaacagaa
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     aaacaaattc cccaaactta caatgatggt atgaaattta attataatag catttctcag
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     caaggaaatc attctaccat tagttatcct aataatacta ttttgatgga tagtcttttt
                                                                           1680
     tcaattaaat acaatattaa taatcaaaat cctcataaat ttggattcca tttaaaacag
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     aaaaacaata agetgeaact ttacaaaaac ttetattete tteetttage aettatgtea
35
                                                                           1800
     aatcatattt acaaagatgt caagtttgac tcttatcccc ttgataatca acaaaaattt
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     gttaatgaat tgacagatct aaatcttaca cttttcaaag aaatccctat tatttcaagt
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     gtcggaatgc aagttttaga taatcgtgtt actattaatg gttcaaaagg aaataaggca
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     caagtttact atactgtaaa gtgtcctgca aatagtcaac tttatatcag ccttcctaac
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     tatatcatag acgaaagtta ttatcttttt aatttaggaa attataaaaa aactcaaaca
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     ttaatattta agcttagttt tccaaaaaat aaaacggtta gttatgattt accacatatt
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     tatgctctcg atttaactgc ctatcaaaaa agtataaagc aattaaaaag tcaaactgtt
                                                                           2280
     aaaacaacaa ctaagaaaaa taaaattttt actacctatg ttgccaaaaa gagaacttcc
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     ttgatttaca ctttaccata tgataaaggt tggtttgcta aacaaaatgg aaaagcaatt
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     aaaatatcta aagcacaaaa tggactaatg aaaattgatg tttctaaagg tagtgggaag
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     attataatga cttttgtgcc ccaaggacta tatcaaggaa ttcttcttac ctgtctaggt
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     atctttctct ttgtatttta ccaactttat tacaaaaaat ttaatttaaa ataa
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     <211> Length : 2574
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           SequenceDescription:
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     actgcttgcg gatcaaaaac atctaaaaaa acagtaaccc ttgcgactgt tggaacaaca
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     aatccatttt cttatgagaa aaagggaaaa ttgacgggat atgatatcga agttgctaag
                                                                            180
     gaagttttca aagcttctga taaatacgat gtcaaatatc aaaaaacaga gtggaccagc
                                                                            240
     attttctctg gtctagatag tgacaaatat caaatcggag ctaacaatat cagttatact
                                                                            300
     aaagagcgtg ccaataaata tctttattct aatccaacgg cttccaatcc attggtatta
                                                                            360
65
     gtggttccaa aagatagtga tattaagtct tataacgata ttgctgggca tagcactcaa
                                                                            420
     gttgttcaag gaaatacaac agtgtctatg ctgcagaaat tcaataaaaa ccatgaaaac
                                                                            480
     aatcaagtta aactaaactt taccagtgaa gatcttqcqc atcaaatccg gaatgtcagt
                                                                            540
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gatggtaagt atgattttaa aatttttgaa aaaatttcag cagaaacgat catcaaagag
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      caaggacttg ataatttgaa agttattgat cttccttcag accaaaaacc atatgtttac
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      tttatttttg cgcaagacca aaaagactta caaaagtttg tcaataaacg tctcaaaaaa
                                                                              720
      ctttacgaga atggtacact tgaaaaaatta tcgaaaaaat accttggagg aagctatctt
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      ccagataaaa aagatatgaa ataa
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      <211> Length: 804
            SequenceName : SEQ ID 602
            SequenceDescription :
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      Sequence
      <213> OrganismName : Streptococcus mutans UA159
      <400> PreSequenceString :
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      gaacggattg attcaaatac agttgctgta aaccctgatt cgctcatttt aaagcgattt
                                                                              120
      ttaaaaacaa atcaattaaa tgggatcatg attgtgacgg ggccagatgg taaggctcaa
                                                                              180
     gtattttcaa atcaaagcaa ggtagatggc agtcctgttt caattaaqqa ttattttcct
                                                                              240
      cttgcttctt tacaaaaatt gataacaggg gtggctatcc aacaattaat tgataaagga
                                                                              300
     aaactgtett taaacacace tttaagcaaa tattateete aaattgaaaa tagtgaaaat
20
                                                                              360
     atcacgatac aaaatttact tacccacaca agcggtttgg cagatcgaaa agaagttcct
                                                                              420
     cagcaagtgc tgacaactca agagcagcaa ttggattttt cattgaccaa ttatcgcgta
                                                                              480
     acttatcgaa aaaaatggaa gtatgctaac attaattatg ctttgctagc tggcattatc
                                                                              540
     agtcaaatta geggtcaaaa ttatgegaet tatgttegte aacaettett aacagetggt
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25
     aaggggtggc attttaaaaa gtatattcaa ataaaagata agtccaagtt agctgccttg
     teagtgatgg ateaaagtac gaettgggat aagetgteaa aagaagtgac atetacettt
                                                                              720
     ggagctggtg attatgcttc taggccagtg gattattgga aatttatgat ggcttttatt
                                                                              780
     aatgaccaat ttgttcctgt cagcgaatac caacgttcta tgaaaatgac ttctaaqaqc
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     tattatggcg gcctctatat cagccaaaag atgctgcatg caaatggtgg tggctttgat acttactctt gttttgctta ttcaaatcct aaaaccaaac aggtcatggt tttgtttatc
                                                                              900
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                                                                              960
     acaaacggta agtataaacg ggtcaaatcc ttagcagcta aagcctttaa actatatgca
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     gattcgtatg cgctgaggaa aaatgaaacg tcaaaataa
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     <211> Length: 1059
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           SequenceDescription:
     Sequence
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     <213> OrganismName : Streptococcus mutans UA159
     <400> PreSequenceString :
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     tgcagctcag cacctggtgg ttcatcagat gcagctggta ataaaattgg agatactgta
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     aaaattggtt acaatcttga attatcagga gatgtagccg cttatggaca agctgaaaag
                                                                              180
     aacggtgcta accttgctgt tgaagagatt aataaggcag gcggcattga tggcaaaaag
                                                                              240
     attaaagtta totcaaaaga taataaatot gataacggtg aagcatcaac aatotcaact
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     aatettgeta eccaaagtaa agtaaatget atettgggae eageaacate tggtgetaca
                                                                              360
     geggetgetg eteceaatge caacgatget geagtaceae tegtaacgee ttetggaaca
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     caagataatt tgacctattc aaaaggcaaa gttcaagatt acatcttccg tacaactttt
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     caagatagct tccaaggaaa gatcattgcc aaatatgcaa cagataattt qaaaqctaaa
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     aaaaaagcat ataaagggaa gattactgtt gaagatacct ttcaaqctaa aqaccaaqat
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     ttccaagcag ctctgaccaa gtttaaaaaat aaagactttg atgccattgt gataccaggt
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     tattatactg aaactggtct gattacaaag caagcacgtg atatggggct tacccagcct
                                                                              780
55
     atcttaggac ctgatggttt taatgatgaa aaatatgttg aaggtgctgg tgcagccaat
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     accaataatg ttcattatgt atctggttac tcaacaaaag ttgctttaac aaataaggct
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     gaaaaattcc tgaaagatta taaggctaag tatggtgaag agccaaatat gtttgccgct
                                                                              960
     cttgcttatg attccgttta tatgattgct gatgctgcaa aagatgccaa aacatctaag
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     gatattgcaa caaacctagc taaattgaaa aactttaaag gtgtgacagg taaaatgaca
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60
     attgataaga aacataaccc tgttaaatca gccgttatgg ttggtcttaa agatggtaaa
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     <211> Length: 1173
           SequenceName : SEQ ID 604
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           SequenceDescription :
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Sequence

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     gatattacta agaatatcgc tggtaataag gttgtcttac atagtatcgt tcctgttggt
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     cgagatecte acgaatatga gcetetteet gaagatgtta aaaagacete teaggetgat
                                                                             240
     gtcatttttt ataatgggat taatcttgaa aatggaggca atgcttggtt taccaaacta
                                                                             300
     gttaaaaatg ctcataaaaa gacagacaag gattattttg cagtgagcga tagtgttaag
                                                                             360
     accatttatt tggaaaatgc aaaagaaaaa ggaaaggaag atcctcatgc ttggcttgac
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10
     cttaaaaatg gtattattta tgctaaaaat atcatgaaac gtctatctga aaaagatcct
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     aaaaacaaga gttattatca gaaaaatttt caagcetaca gcgccaaact tgaaaaacta
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     cacaaagtag ccaaagaaaa aatcagtcgt atccctactg agaagaaaat gatcgtaact
     agrgaaggtt gtttcaagta tttctctaag gcttacgata ttccttctgc ctatatatgg
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     gaaattaata ccgaagaaga gggaacacca aatcaaatta aggctttagt gaaaaaatta
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     aggaaaagtc gggtgtctgc gctttttgta gaaagcagtg ttgatgatcg tccaatgaaa
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     actgtttcaa aagatacagg tatcccaatt gccgctaaaa tttttacaga ttcagttgct
                                                                             840
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     aaaaaaggac aggctggaga tagttactat gcgatgatga agtggaatat agataaaatt
     gcaaatggtc tgtcacaatg a
                                                                             921
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     <211> Length : 921
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           SequenceDescription :
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     <400> PreSequenceString :
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     ctgcttcttt ttttattgcc tattgtgtca gtattggctt ttattgtgtt atttattggc
30
                                                                             120
                                                                             180
     qqtqqtacaq ctqaqtctca tqatgtggaa gcgacgacag ggggcgttaa gctttcagct
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     aagcaatttg cagataagac aaagttagga atttcagaag aggaagctaa aaatgcctta
     gettttgegg ataggttgat gtetegteat eattttaeag eteaageaac tgetggagta
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     ttggctgttg gctttcgtga aagtggcttt gatgtcaaag cagttaataa ttctggtggt
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     gtagetgget ttttccaatg gtetggetgg ggtagttetg ttaatggtga tegttggaaa
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                                                                             420
                                                                             480
     gtagctagta aaagagagtt aactctagag gttgaggtag atttgatgag cactgaacta
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     gatggtcgat atgctgatgt tgtcaaaaaa gttggttctg cgactgatga aaaacaggct
     gctaaggatt ggtctcagta ttatgaaggt gttgcggtta gtgatggtca aacgaaagct
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     gataaaattg agagttgggc aacaactatt tgtgaggctt taaagtctgg tggtacaaat
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     tatgctaaag tgaataatac gggaacaagt tctactgcta tcccgcaggg ttgggaaaat
     attagtgett ttgatggeca tgettatgaa ggtagtgaaa attateetea aggacaatge
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     acttggtatg tttataatcg tgctaaacag ttgggtgtta gcttcagtcc ttatatgggg
                                                                              840
     aatggeggte agtggtatea agtgeaagge taccatteta gteatacace taaageacat
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     acggetttat etttgteaa tggteaggea ggttetgate caacttatgg teatgttget
tttgtagagg etgttaaaga tgatgggagt attetaatea gtgagatgaa egtttatggt
                                                                             960
                                                                             1020
45
     caaccagcta tgacggttgc ctatcggaca tttgatgctg aaactgctaa acaattttgg
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     tatgtagagg gaaaataa
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     <211> Length: 1098
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           SequenceDescription :
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     atcacaaaat cagatggtac agcactttct aatgatccat ctaaggctgt taattattgg
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     qaaccacttt ctttcagtaa ttctattact ttcccagatg aagtcagtat taaggctggg
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     gatactttaa ccattaagtt gccagagcaa ttacaattta cgactgctct aactttcgat
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△ 360

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	cocgectacg acactacege caccaccaaa teegaegege tetecagegt	acacagotac	300
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	5 55 acception accepted acceptate togular contact to	cyacytatic	600

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Sequence

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# WO 2005/076010 PCT/IN2005/000037 275/341

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## Sequence

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40 45 50	<pre>&lt;213&gt; Organ &lt;400&gt; PreSe gtgccagctt accgacagcg cctggcgtca aatgcgcaaa acgcttggcg gtccaggtctgc caggtctgc caggcgctgg gtgattaaca gttccggcgg actaacacag gtgcgattt gcagattta gcagattt gcagattta acctttggcg gtacccacag gtgcgattt gcagattta ccgacgctg agcactatta ccgacgcttg aatccgtta</pre>	equenceStrine ccgcagtagg caggcaacag ccattaaccc ccatcagcgg ggaaaactta cggatattca ttggcaatac gcgttgacac tgataactgg cggtcactta cagacgtgag ccggaacaac ccattaacac cccttccgg ggaaaaccta acggcaacac ccattaacac ccatcagcgg	tggetggge caatteegee agttgegace ceaggtgacg cacegetace ggceategge tggeageggt cgtgeagege tageageage tageageage taacegetace getteegge categacet accaceate cgttteegge cacegetace cgtgttacge ggettegga categeace tategeace tategeace tategeace tategeace tategeace tategeace tageacece tageacece tageacece	gaagccagct agccataacg gacgatatta ggggcggcgg gtgcagggga aatggcaatc tcgcgagata gatgatgtgg ggctggcgg gtattagccg gcgggtacgg gacgatgtga ggcgtggaag gtagcgggcg gacggcgacg acccacgcct gacgatattc gacgatattc gacgatattc	acacggtgac tgcaggtcaa ttaacgccgc cgggcgatac atttaagctg tgacggttaa ttactatcga tcactatcga tcaggcgcggc atggcacatg tgaatatcac tcaccgtcga ttaacgccgc tggggcaaac atggtagctg ccaccgtgca acagcgtcga tgaacgctgc ggcagacggt	taccgcgctg cgaatcggc ggttaccgta gagcgtggac cgcttcggtg cgacacctg gagcgttggt gataagtggt gataagtggc tctggcggcg cgaaaaaggg ggtcaccgtt gacaaccacc ggccagcgtc tgccagggc	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140
40 45 50	<pre>&lt;213&gt; Organ &lt;400&gt; Press gtgccagctt accgacagcg cctggcgtca aatgcgcaaa acgcttggcg gttccggcgg accaacggcg ccaggtctgc caggcgttgc gtgattaaca gttccggcgg actaacacag gtgattaaca gttgcgatt gcagattta acctttggcg gtaccagcgc agcactatt accgacgcttg agcactatta ccgacgcttg aatccgttg</pre>	equenceStrine ccgcagtagg caggcaacag ccattaaccc ccatcagcgg ggaaaactta cggatattca ttggcaatac gcgttgacac tgataactgg cggtcactta cagacgtgag ccgttaacac ccattaacac ccctttccgg ggaaaacta ccgatctcag acggcaacac ccattaacac ccattaacac ccattaacac ccattaacac ccattaacac ccatcagcgg tgacttacag tgacttacag	tgg: tgggctgggc caattecgcc agttgcgacc ccaggtgacg caccgctacc ggccatcggc tggcagcggc tagcagcagc tagcagcagc cataccatc cgtttccggc caccaccatc cgtttccggc caccacccccatcccccgttaccc cgtgttaccc	gaagccagct agccataacg gacgatatta ggggcggcgg gtgcagggga aatggcaatc tcgcgagata gatgatgtgg gtattagccg gcgggtacgg gcaccatccgg gacgatgtga ggctggaag gtagcgggcg gacggcgacg acccacgcct gacgatattc gccgaagcgg caggcgacg	acacggtgac tgcaggtcaa ttaacgccgc cgggcgatac atttaagctg tgacgttaa ttactatcga tcactatcga tgaatatcac tcaccgtcga ttaacgccgc tggggcaaac atggtagctg caccgtgca acagcgtcga tgaacgctgc ggcagacggt	taccgcgctg cgaatcggcc ggttaccgta gagcgtggac cgcttcggtg cgcaacctg cgagcacgct gatgacggtg gagcgttggt gataagtggc tctggcggcg cgaaaaaggg ggtcaccgtt gacaaccacc ggccagcgtc tgccagggcc agagcggcc aaccgtcaccg cgtcagcgtc accgtcaccg cgtcagcgtc	120 180 240 300 360 420 480 540 600 720 780 840 900 960 1020 1080
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40 45 50	<pre>&lt;213&gt; Organ &lt;400&gt; PreSe gtgccagctt accgacagcg cctggcgaa aatgcgcaaa acgcttggcg gttccggcgg accaacggcg ccaggtctgc caggcgttgc gtgattaaca gttccggcgg gtgattaaca gttccggcgg actattggcg gtactacacag gtggcgattt gcagatttaa acctttggcg gtacccgccg agcactatta ccgacgcttga atccgttaa cttaatggtg ccgacggcgg gataaagcgg</pre>	equenceStrix ccgcagtagg caggcaacag ccattaaccc ccatcagcgg ggaaaactta cggatattca ttggcaatac gcgttgacac tgataactgg cggtcactta cagacgtgag ccgttaacac ccattaacac ccattacag ggaaaaccta ccgatctcag acggcaacac ccattaacac ccattaacac ccattaacac dcatcagcgg tgacttacag atgacttacag atctcagcaa gtaacccggc	tggetggge caatteegee agttgegace caegetace ggecategge tggeageggt egtggegge tageageage cgetgeaaca taactggeet atcaecate cgttteegge cageacetee cacegetace ggetteegee categecace categecace tggetgeace categecace categecace tageageace cgtgttacge ggetteegea categecace tageageace tegeeteegte tetgaeegec gteegetaac	gaagccagct agccataacg gacgatatta ggggcgggggga atggcaggga aatggcaatc tcgcgagata gatgatgtgg ggattagcgg gtattagccg gcggtaccgg gcggtggaag gacgatgtga ggcgtggaag gacgacgacg acccacccct gacgatattc gccgaagcg acccagcct gacgatgtca acccagcct gacgatgtca acccacgcct cacgacgacga caggcggacg acccagcg	acacggtgac tgcaggtcaa ttaacgccgc cgggcgatac atttaagctg tgacggttaa ttactatcga tcaatagcat cgggcgcggc atggcacatg tgaatacac tcaccgtcga ttaacgccgc tggggcaaac atggtagctg ccaccgtgca acagcgtcga tgaacgctgc ggcagacgctg gcagacgctg gcagacgctg gcagttggag ccgttagtgc cggtggatct	taccgcgctg cgaatcggcc ggttaccgta gagcgtggac cgcttcggtg cgccaacctg cgagcacgct gctgacggtg gagcgttggt ggtaagtggc tctggcggcg cgaaaaaggg ggtcaccgtt gacaaccacc ggccagcgc cgaagcggcc cgagggggc cgaggggc cgagggggc accgttcaccgtt accacgtcacg cgtcagctta ctcggtaagc catcgtcacg	120 180 240 300 360 420 480 540 660 720 780 840 900 960 1020 1080 1140 1260 1320
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     geccegeaga eggtggegee ggeteegeag eegeegteeg gtggeegeaa eggeagegge
                                                                             1620
     gggggcgact tattcggcgg gttctga
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25
     <212> Type : DNA
     <211> Length : 1647
            SequenceName : SEQ ID 703
            SequenceDescription :
30
     Sequence
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     <400> PreSequenceString :
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35
     teaccageeg gtategeeaa tgeegaegae gegggettgg acceaaaege egeageegge
                                                                              120
     ccggatgccg tgggctttga cccgaacctg ccgccggccc cggacgctgc acccgtcgat
                                                                              180
     actecgeegg eteeggagga egegggettt gateceaace teeceegge getggeeegg
                                                                            . . 240
     gacttcctgt ccccgcctgc ggaggaagcg cctcccgtgc ccgtggccta cagcgtgaac
                                                                             1:300
     tgggacgcga tcgcgcagtg cgagtccggt ggaaactggt cgatcaacac cggtaacggt
                                                                              360
40
     tactacggcg gcctgcggtt caccgccggc acctggcgtg ccaacggtgg ctcggggtcc
                                                                              420
     gcggccaacg cgagccggga ggagcagatc cgggtggctg agaacgtgct gcgttcgcag
                                                                              480
     ggtatecgcg cetggeeggt etgeggeege egeggetga
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     <212> Type : DNA
     <211> Length: 519
45
           SequenceName : SEO ID 704
           SequenceDescription :
     Sequence
50
     <213> OrganismName : Mycobacterium tuberculosis H37Rv
     <400> PreSequenceString :
     atgacgcggc tgataccggg ttgcacgctc gtcgggctga tgctgacgtt actgcccgcg
                                                                               60
     cccacetegg eggeegggag caacacegec accaceetgt teceggtega egaggteace
                                                                              120
     cagetggaga egeacacett cetegattge caceceaaeg geagetgega ettegteget
                                                                              180
55
     ggagcaaatc tgcgcacacc cgacggcccg acgggctttc cgcccgggct gtgggcgcgc
                                                                              240
     caaaccaccg agatecgtte gacgaaccgg ttggcctate tqqacqcqca cqccaccaqc
                                                                              300
     cagttcgaac gggtaatgaa ggcgggcgga tccgacgtga tcaccaccgt ctacttcggc
                                                                              360
     gagggteege eggacaaata ceagaceace ggggteateg actegaceaa ttggtegace
                                                                              420
     ggtcaaccga tgaccgacgt caacgtcatc gtgtgtacac acatgcaggt ggtctacccg
                                                                              480
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     ggggtcaacc tcacctcgcc cagcacctgc gcgcaagcca acttttccta g
     <212> Type : DNA
     <211> Length : 531
           SequenceName : SEQ ID 705
65
           SequenceDescription:
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Sequence

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<213> OrganismName : Mycobacterium tuberculosis H37Rv
      <400> PreSequenceString :
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     atcgtatgca cggtgttcat cgaaaccgcc gttgtcgcga ccatgtttgt cgcgttgttg
                                                                           120
     ggtctgtcca ccatcagctc gaaagccgac gacatcgatt gggacgccat cgcgcaatgc
                                                                           180
     gaatccggcg gcaattgggc ggccaacacc ggtaacqqqt tatacggtgg tctqcaqatc
                                                                           240
     agccaggega cgtgggatte caacggtggt gtcgggtcgc cggcggccgc gagtccccag
                                                                           300
     caacagatcg aggtcgcaga caacattatg aaaacccaag gcccgggtgc gtggccgaaa
                                                                           360
10
     tgtagttctt gtagtcaggg agacgcaccg ctgggctcgc tcacccacat cctgacgttc
                                                                           420
     ctcgcggccg agactggagg ttgttcgggg agcagggacg attga
                                                                           465
     <212> Type : DNA
     <211> Length: 465
          SequenceName : SEQ ID 706
15
           SequenceDescription :
     Sequence
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20
     <400> PreSequenceString :
     atgatgcaac aagcggtgtc gggcattacc ggcgcgctcg gcggcgcggt cggcggcgtc
                                                                            60
     atgggcccac tcacgcagct tccccagcag gccatgcaag cggggcaggg agcaatgcag
                                                                           120
     ccgctgatga gtgcgcttca acagacctat ggcgcggagg gactggacgt cgcggacggg
                                                                           180
     gcgcggctgg tggacagcat cgaaggtgag cccggcctcg gcggcgagcc gggcgctggt
                                                                           240
25
     gacgtcggcg ccggcggcgg gggtggtggc accaccccga cgggctatct gggtccccca
                                                                           300
     cccgtgccga cgtcgtcgcc accgacgact ccagccgggg cgccggccaa gtcggtgacg
                                                                           360
     ceggaceegg ttagtggcac ceeggggeg teggggeegg ceggcatgac eggcatgeeg
     atggtgccgc cgggcgcgtt gggtgcgggc gcggaaggag ccaataagga caagccggtc
                                                                           480
     gagaagcggg tgacgggctg tgccgaatgg tcaaccggtc aagggccgct taacagtacc
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     600
     gateettgtt gtgeegaacg acgacaaggt taa
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     <212> Type : DNA
     <211> Length: 633
           SequenceName : SEQ ID 707
35
           SequenceDescription :
     Sequence
     <213> OrganismName : Mycobacterium tuberculosis H37Rv
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     <400> PreSequenceString :
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     gtcgcgggcg cagacccgca gcgttatgac ggcgatgtgc cgqqqatqaa ctatqacqct
                                                                           120
     tegetgggeg ceccatgete cagetgggag egetteattt ttggacgagg ceceteeggt
                                                                           180
     caggecgaag cetgteattt teegeeteet aaccagttee egeeggeega aaccagetae
                                                                           240
45
     tgggtgatct cctacccgct atacggcgtc cagcaggtcg gtgcgccgtg tccgaagccg
                                                                           300
     caggoggoog ogcagtotoc ggatgggttg cogatgctgt gtotgggago cogtggatgg
                                                                           360
     cageegggat ggtttacegg ggeegggtte tteeeteegg ageeataa
                                                                           408
     <212> Type : DNA
     <211> Length : 408
50
          SequenceName : SEQ ID 708
           SequenceDescription:
     Sequence
55
     <213> OrganismName : Mycobacterium tuberculosis H37Rv
     <400> PreSequenceString :
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                                                                            60
     acceptgatga teatceptggt gttegggeag gtgeggttee ateacaccae egggtactee
                                                                           120
     geggtgttca cecatgtcag egggetgegg geegggeaat ttgteegege tgegggegta
                                                                           180
60
     gaggtcggca aggtcgccaa ggtaacgctg atcgacgggg acaagcaagt attggtggac
                                                                           240
     ttcaccgtgg atcgctcgct gtcactggat caggcgacga ccgcctcgat ccgctacctc
                                                                           300
     aacctgatcg gcgaccggta ccttgagctc ggccgcggtc acagcggtca gcggctggcg
                                                                           360
     cegggtgcca egateceget egagcacace cateeggeet tggatetega egetetgete
                                                                           420
     ggcgggtttc gcccactctt ccaaacgttg gacccagaca aggtcaacag catcgcctcc
                                                                           480
65
     tegateatea eegtgtteea agggeaagge gecaccatea acgaeateet egaeeagaee
                                                                           540
     gcctcgctga cggcaacgct ggccgaccgg gaccatgcga taggtgaggt cgtcaacaac
                                                                           600
     ttgaacaccg tgctggccac caccgtcaag catcaaacgg aattcgaccg cacggtcgac
                                                                           660
```

```
aagetagagg tgetgateae tggaetgaag aacagggegg accegetgge egeggeggeg
                                                                             720
     gcacacatca gcagcgccgc gggaacccta gccqacctqc tqqqqcqqat cqtccattqc
                                                                             780
      tgcacagcag cttcgggcac ctcgagggca tccagcagcc gctcatag
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     gtgagcgcac,ccgccggcgg tcgtgccgcg catgcggatc cgtgttcgga catcgcggtc
                                                                             120
15
     gttttcgctc gcggcacgca tcaggcttct ggtcttggcg acgtcggtga ggcgttcgtc
                                                                             180
     gactcgctta cctcgcaagt tggcgggcgg tcgattgggg tctacgcggt gaactaccca
                                                                             240
     geaagegacg actacegege gagegegtea aaeggtteeg atgatgegag egeceacate
                                                                             300
     cagegeaceg tegecagetg ecegaacace aggattgtge ttggtggeta ttegeagggt
                                                                             360
     gcgacggtca tcgatttgtc cacctcggcg atgccgcccg cggtggcaga tcatgtcgcc
                                                                             420
20
     getgtegeee tttteggega gecateeagt ggttteteea geatgttgtg gggeggeggg
                                                                             480
     tegttgeega caateggtee getgtatage tetaagacea taaaettgtg tgeteegae
                                                                             540
     gatccaatat gcaccggagg cggcaatatt atggcgcatg tttcgtatgt tcagtcgggg
                                                                             600
     atgacaagcc aggeggegac attegeggeg aacaggeteg ateaegeegg atga
                                                                             654
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     <212> Type : DNA
     <211> Length: 654
           SequenceName : SEQ ID 710
         · SequenceDescription :
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     Sequence
     <213> OrganismName : Mycobacterium tuberculosis H37Rv
     <400> PreSequenceString :
     gtgataagca ccacaagaat tgatttccta tggatattgt cggtagcgtt cgcgtccatg
35
     attgctcttg caacgctgtt gacgcttatc aatcaagtcg tcggcactcc gtatattccc
                                                                             120
     ggtggcgatt ctcccgccgg gaccgactgc tcggagctgg cttcgtgggt atcgaatgcg
                                                                             180
     gegaeggeea ggeeggtttt eggagatagg tteaacaceg geaacgagga ageegeettg
                                                                             240
     geggeteggg gettteaaca gggaacegee eccaatgeet tggtgategg ttggaatgge
                                                                             300.
     caccacacgg cggtgacgct gcccgatggc acgcccgtat ccagtggtga aggcggtggc
                                                                             360
40
     gtgcgggtcg gtggcggtgg cgcctaccag cccaaattca cccaccacat gtatctgccg
                                                                             420
     atggatgtgg acgcgggaga agaccagccg ccggcgccag atgagccggt caccgcggtc
                                                                             480
     gacgacgtgg aaccggaaat gcctgcaccg tgcccgaccc agcgcccgcc ggtgaccccg
                                                                             540
     agacataacc tgtgcaacaa actccggact atgccagggg cgctctcggc cgcgctggcc
                                                                             600
     geggeggege eggtetggee ggeceetata ageggetgee gegggtteag eacgteeete
                                                                             660
45
     ttagcaaaaa gaaatcaccc agtaatcgtc gggaaatag
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     <212> Type : DNA
     <211> Length: 699
           SequenceName : SEQ ID 711
           SequenceDescription :
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     Sequence
     <213> OrganismName : Mycobacterium tuberculosis H37Rv
     <400> PreSequenceString :
55
     atgacgacga tgattactct tcggcgacgg ttcgcggtgg ccgtcgccgg cgtcgccact
     geogeogega egacegteae eetggeteee geaceageaa atgeogeega tgtetatgge
                                                                             120
     gcaattgcct actccggcaa cggctcgtgg ggccgatcgt gggactaccc aacccgggcg
                                                                             180
     getgeegaag ceacegeegt caagtegtgt ggetacteeg actgeaaggt geteaceagt
                                                                             240
     ttcaccgcct gcggcgccgt cgccgccaac gatagggcat accagggagg agttggaccc
                                                                             300
60
     accttggccg ccgccatgaa ggacgccctg accaagctcq qcqqcqcta catcqacacc
                                                                             360
     tgggcctgca actaa
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     <212> Type : DNA
     <211> Length: 375
           SequenceName : SEQ ID 712
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           SequenceDescription :
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Sequence

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    atggccggac tgaacattta cgtgaggcgc tggcggacag cgcttcacgc aaccgtgtcg
                                                                            60
     geattgatag ttgccatect eggactegee atcaceegg tegetagtge ggegaeggee
                                                                           120
     agggcgacgt tgtcggtgac atcgacgtgg cagaccggtt tcatcgcccg cttcaccatc
                                                                           180
     acaaactcga gcacggcgcc gctaaccgat tqqaaqcttg aattcgactt gccggcagga
                                                                           240
     gaatccgtct tgcacacatg gaatagcacc gttgcacgat ctggcacgca ctacgttctc
                                                                           300
    agcccagcga attggaatcg catcattgcc cccggtggtt cagccacggg cggcctaaga
                                                                           360
10
    ggcgggctga ccggttctta ctcgccgccg tcgagttgtc tgctcaacgg gcaatatcct
     tgcacctag
                                                                           429
     <212> Type : DNA
     <211> Length : 429
          SequenceName : SEQ ID 713
15
         SequenceDescription :
     Sequence
     <213> OrganismName : Mycobacterium tuberculosis H37Rv
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     <400> PreSequenceString :
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     gtggtggtcc ttggttggta tttcctgcgg atacccagcc tggtcggcat cggtcgatac
                                                                           120
     acgetttatg ccgaattgce tcggtccggg ggtctatacc gaacagccaa cgtcacatat
                                                                           180
                                                                           240
     cggggcatca ccatagggaa ggtcaccggc gtcgaaccaa ccgagcgggg cgcgcgagca
25
     accatgagea tegacaatgg ctaccagate eccacegacg ceteggeeaa tgtgcactea
                                                                           300
    gtgtcggcgg tcggcgagca gttcgttgac ctggtgtcga cccgcaccag cggtccgtat
                                                                           360
     ctgcggcatg ggcagacgat caccacgact acggtcccca gccagattgg cccggcgctg
                                                                           420
     gacgccgcca accgtggatt ggcagtgctg cccaaagacc gggtcgcgtc ggtgctgcac
                                                                           480
     gaggegtegg aggeegtegg egggetggga teeteactga ategeeteat egaageeace
                                                                           540
30
     caggcaatcg cccacgatgt caggggcagc ctcgaggaca tcgacgacat catcgagggt
                                                                           600
     teggegeeta teategatag eeaggteaat teeggeaacg agategeeeg etgggeegee
                                                                           660
                                                                           720
     aacctcaaca cgctggccgc tcagaccgcg cagaccgatc cggcggtgcg aagcattctg
    gccaacgcgg caccgactgc cgatcaggtc aacgccacgt tcagcgacgt gcgggagtcg
                                                                           780
                                                                           840
     ttgccgcaga cgctggccaa tctcgaggtc gtaatcgata tgctcaagcg ctaccacaac
35
    ggcgtcgagc aggcgttggt gttcttgccg cagtccggcg cgatcgccca gtcggttact
                                                                           900
     acagagttee ceggecagge eggactgggt gteggeggee tggegeteaa ceaaceaceg
                                                                           960
     ccgtgcctga ccggcttcct gccggcgtcg gagtggcggt cacctgctga caccagcacc
                                                                          1020
    geacegetae ceaagggeae etactgeagg attecgatgg aegegageaa tgtggttegt
                                                                          1080
     ggagcacgca acaacccgtg tgtagacgtg cccggcaagc gggcggcgac cccgcgggaa
                                                                          1140
     tgccgcagca atgaagctta tgtgcccggg ggcaccaatc cctggtatgg ggaccccaac
40
                                                                          1200
     cagatgetea getgteeege geeggeegeg egttgtgace ageeggtgaa geeaggeeag
                                                                          1260
     gtgatcccgg cgccgtcagt taacaatggc atcaacccgc tgcccgccga tcagctgcca
                                                                          1320
    ggcacacctc caccggtcaa cgatcctttg cagcgacctg ggtcaggcac cgtccagtgc
                                                                          1380
                                                                          1440
     aatgggcaac aacccaaccc gtgcgtctac accccgagca catttcctac aaccatttac
    gacgtgcaga gcggcaaagt cgtagcaccc gacggtgtgg tgtattccgt tgaggcttcg
45
                                                                           1500
                                                                          1551
     actcatgccg gagccgacgg atggaaggtg atgctggcac caaccggctg a
     <212> Type : DNA
     <211> Length : 1551
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           SequenceName : SEQ ID 714
           SequenceDescription :
    Sequence
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     <213> OrganismName : Rickettsia prowazekii strain Madrid E
     <400> PreSequenceString :
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     atgagttcta taaaaaatac cactaatcta gatctttcat ctatcaccaa tacaattcaa
                                                                            180
     aaaqccatqa atattttttt taccactaac aaaatttcca caqaaaqtat gcaatctttg
60
     tttaagaaaa attccgagat tatacaaaat aatattaata ctattttaaa tagtactaaa
                                                                            240
    gaagtaataa attctaaaga ttttaaacaa gctactgaat atcatcaaaa atgtgtaaaa
                                                                            300
     tctatttatg aaacatctat ggacaatgct aaggaattag caaatattgc ttatgaagct
                                                                            360
     tcaaataaaa tatttgaagc cgcaaataaa catattacca agaatattca taatgcttct
                                                                            420
     aataatatac ataatactgc agaacaagta caaaaaaact ttaataacaa atctgcttaa
65
     <212> Type : DNA
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<211> Length: 480

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SequenceName : SEQ ID 715
SequenceDescription :

```
Sequence
 5
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     gatttaaatc atattcaaga tagttttaaa tatcaagaag cagagcagtt aacaatagaa
                                                                          120
10
     ttaccttgga atgactgtac tgcaattcat aaattcttag aagaaaagtt attttttca
                                                                          180
     gaacaacaaa taaaaaaaga aaataaaatt catgagaaat ataagcaatt ttatttacaa
                                                                          240
     cataataata agctttctga tttttctatg caatttctag aaaaaaaatc tgaaattaat
                                                                          300
     agtgtcgaaa ctttaatatc aggcttttta aaattttgtg aagataattt tcaaacaagt
                                                                          360
     assagtsaat cgcattcttt asattttttc casassacas asgaccastg gttacatast...
                                                                          420
15
     ataagaaatg agaattataa aacatattat aagaagaaat atgaagacaa tacctttaga
                                                                          480
     aatattaatt aa
                                                                          492
     <212> Type : DNA
     <211> Length : 492
          SequenceName : SEQ ID 716
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          SequenceDescription :
     Sequence
     <213 > OrganismName : Rickettsia prowazekii strain Madrid E
     <400> PreSequenceString :
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     tttgcagagt gcattgataa tgaatggtat ttaagagcag atgcaggtgt agcaatgttt
                                                                          120
     aataaagaac aagataaggc aacaggtgtt aaattaaaat ctaataaggc tattccaatt
                                                                          180
     gatttgggta ttggttatta tatttctgaa aatqtacqtq ctqatttaac tttaqqaact
                                                                          240
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     acaataggtg gaaaactcaa gaaatacgga gcagcaacta atacacattt tactggtact
                                                                          300
     aacgtttcag tgagccataa gcctactgtt acacgtttgc ttattaacgg ttatgtagac
                                                                          360
     ttaacaagtt ttgatatgtt tgatgttttc gttggtggtg gtgtcggtcc tgcattagtg
                                                                          420
     aaagagaaaa ttagtggggt aagcggtctt gcatctaaca ctaaaaataa aaccaatgta
                                                                          480
     tcatataagc tgattttcgg tacttctgcg caaattgcag atggtgttaa agtagaqcta
                                                                          540
     600
     agtgtgcaaa ccggtggtat gcgttatcaa agtcataacc tgacagtagg tgtaagattt
                                                                          660
     ggtatataa
                                                                          669
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     <211> Length: 669
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          SequenceName : SEQ ID 717
          SequenceDescription :
     Sequence
45
     <213> OrganismName : Rickettsia prowazekii strain Madrid E
     <400> PreSequenceString :
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                                                                           60
     ttattaagca gttgctccga atctacgcgt gatgaaaatg gattacttac agatagtcaa
                                                                          120
     agtactataa ttcgagatta tataatatcg caaaattcta aaaatcttaa agtgaacctt
                                                                          180
50
    aaagaaaagt ttggttccaa tttaaaagga gtaaaattaa taggaataaa gttaacaaat
                                                                          240
    gaagatttat cgggaataga tttcacttca tgcgaaatat tacggactga cttcatgggt
                                                                          300
     agcaacttag aaaaagcaat acttacaaat teggtaatte aagaaagtaa ttttgeggat
                                                                          360
     tcagtaataa aaaatatttc aggctataat gctgattttc aaggttcaat ttttaataat
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     ataacattac aaaatacaaa ttttgttcaa tcaaatttca gtgatactgc ttttaataaa
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55
     agtactataa tcaatgtcaa ttttgaaaat tctaaattta gtaatgtatt atggtgtcac
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     agtaatattg acagtagtaa ttttcaaaaa actcatctaa aaaataatag ctttaaaaaat
                                                                          600
    actaatgtaa tgaattcaat attttatggt gcagatttag gcaaaagtgt aataaataat
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    acaaatttta ctaataatta ttttgaatct agtgacctaa gtaacactaa attcacatca
                                                                          720
    gtaatcatta aagattotaa ottoacacaa agtattttta attoagtaaa tttoaataat
                                                                          780
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    atacaaagta ataactcttt tttttcatat acttcctttg aagattcaac attacacaat
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    attcacctta ctaaatgtga tttacaaaac agcacaatta atagttcagt tttcaataat
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    tttaaaaatcg acaatgctat attaacaaat atgagtctca acgataatac atttaataat
                                                                          960
    ttatcaataa aaaatagtaa tactaatttt gtaaggatta ataaatccaa agggtttaat
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    attactttac tcaatactaa ctatagtaat gctattttta gcaataatga tttaaaagaa
                                                                         1080
    tttaaagtca ttaatactga tttaaacaac agtgaaataa taaactcaaa tttcactaat
                                                                         1140
    ggacaattta ataatgtaaa tttttctcaa tctttaatac aaaacgtaaa ttttacagac
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# WO 2005/076010 PCT/IN2005/000037 320/341

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## WO 2005/076010 PCT/IN2005/000037

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                                                                            1020
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                                                                            1140
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SequenceDescription :
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     Sequence
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40
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     <211> Length : 660
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SequenceName : SEQ ID 763 SequenceDescription :

45

# (19) World Intellectual Property Organization

International Bureau



# 

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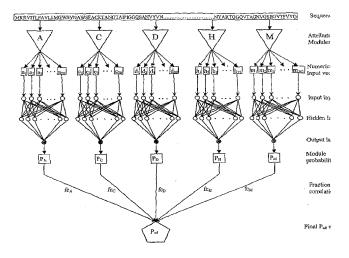
Mall Road, New Delhi 110 007 (IN). **RAMACHAN-DRAN, Srinivasan** [IN/IN]; Institute of Genomics and Integrative Biology, Mall Road, Dehli 110 007 (IN).

- (74) Agents: BHOLA, Ravi et al.; K & S Partners, 84-C, C6 Lane, Off Central Avenue, Sainik Farms, New Delhi 110 067 (IN).
- (81) Designated States (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.
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[Continued on next page]

(54) Title: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE PROTEINS OF THERA-PEUTIC POTENTIAL

#### The Neural Network architecture



(57) Abstract: A computational method for identifying adhesin and adhesin-like proteins, said method comprising steps of computing the sequence-based attributes of a neural network software wherein the attributes are (i) amino acid frequencies, (ii) multiplet frequency, (iii) dipeptide frequencies, (iv) charge composition, and (v) hydrophobic composition, training the artificial neural Network (ANN) for each of the computed five attributes, and identifying the adhesin and adhesin-like proteins having probability of being an adhesin ( $P_{ad}$ ) as  $\geq 0.51$ ; a computer system for performing the method; and genes and proteins encoding adhesin and adhesin-like proteins.



## WO 2005/076010 A3



### **Declaration under Rule 4.17:**

 as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))

#### Published:

with international search report

# (88) Date of publication of the international search report:

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

Inte nal Application No

		PC1/1N2	005/00003/
	G06F19/00 G01N33/68	ii-n and IBC	
	o International Patent Classification (IPC) or to both national classific	ation and IPC	
	SEARCHED cumentation searched (classification system followed by classification)	ion symbols)	
	G06F G01N		
	tion searched other than minimum documentation to the externt that state at a base consulted during the international search (name of clata ba		
	ata base consulted during the international search (name of Gata ba	ise and, where practical, scaron come	ea)
C DOCUME	ENTS CONSIDERED TO BE RELEVANT		
Category °	Citation of document, with indication, where appropriate, of the rel	levant passages	Relevant to claim No.
Galege.,	Citation of decement,		
A	ZUEGGE J ET AL: "Deciphering ap targeting signals - feature extrement from nuclear-encoded precursors Plasmodium falciparum apicoplast GENE: AN INTERNATIONAL JOURNAL O AND GENOMES, ELSEVIER, AMSTERDAM vol. 280, no. 1-2, 12 December 2001 (2001-12-12), p 19-26, XP004313161 ISSN: 0378-1119 the whole document	raction of proteins" N GENES , NL,	1-13, 18-21
X Furth	ner documents are listed in the continuation of box C.	X Patent family members are liste	d in annex.
"A" docume consict "E" earlier d filling d: "L" docume which i citation "O" docume other n	nt which may throw doubts on priority claim(s) or is cited to establish the publication date of another or or other special reason (as specified) ent referring to an oral disclosure, use, exhibition or neans or other prior to the international filing date but	"T" later document published after the ir or priority date and not in conflict wincited to understand the principle or invention  "X" document of particular relevance; the cannot be considered novel or cannot be considered novel or cannot be considered novel or cannot be considered to involve an document of particular relevance; the cannot be considered to involve an document is combined with one or ments, such combination being obvin the art.	ith the application but theory underlying the eclaimed invention not be considered to document is taken alone eclaimed invention inventive step when the more other such docurious to a person skilled
later th	an the priority date claimed	"&" document member of the same pater	
	actual completion of the international search  November 2005	Date of mailing of the international so	·
Name and ra	nailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Authorized officer  Lüdemann, S	

Inte nal Application No
PCT/IN2005/000037

C.(Continua	ation) DOCUMENTS CONSIDERED TO BE RELEVANT	
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	BRADLEY PHIL ET AL: "BETAWRAP: Successful prediction of parallel beta-helices from primary sequence reveals an association with many microbial pathogens" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, vol. 98, no. 26, 18 December 2001 (2001-12-18), pages 14819-14824, XP002350912 ISSN: 0027-8424 the whole document	1-13 , 18-21
A	FINLAY R BRETT ET AL: "Common themes in microbial pathogenicity revisited" MICROBIOLOGY AND MOLECULAR BIOLOGY REVIEWS, vol. 61, no. 2, 1997, pages 136-169, XP002350913 ISSN: 1092-2172 the whole document	1-13 <b>-</b> 18-2 <b>1</b>
Р,Х	SACHDEVA GAURAV ET AL: "SPAAN: a software program for prediction of adhesins and adhesin-like proteins using neural networks" BIOINFORMATICS (OXFORD), vol. 21, no. 4, 15 February 2005 (2005-02-15), pages 483-491, XP002350914 ISSN: 1367-4803 the whole document	1-13 18-2 <b>1</b>
E	WO 2005/057464 A (COUNCIL OF SCIENTIFIC AND INDUSTRIAL RESEARCH; BRAHMACHARI, SAMIR, KUM) 23 June 2005 (2005-06-23) the whole document	1-13 - 18-2 <b>1</b>

.....national application No. PCT/IN2005/000037

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)
This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)
This International Searching Authority found multiple inventions in this international application, as follows:
see additional sheet
As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
As all searchable claims could be searched without effort justifying an additional fee, this Authority dict not invite payment of any additional fee.
3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:  1-13, 18-21
Remark on Protest  The additional search fees were accompanied by the applicant's protest.  No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-13, 18-21

A computational method for identifying adhesin and adhesin-like proteins comprising the steps of claim 1.

Invention 2-275: claim 14

A set of 274 annotated genes encoding adhesin and adhesin-like proteins, having seq. id nos. 385 to 658.

Invention 276-380: claim 15

A set of 105 hypthetical genes encoding adhesin and adhesin-like proteins, having seq. id nos. 659 to 763.

Invention 381-659: claim 16

A set of 279 annotated adhesin and adhesin-like proteins, having seq. id nos. 1 to 279.

Invention 660-764: claim 17

A set of 105 hypothetical adhesin and adhesin-like proteins, having seq. icl nos. 280 to 384.

Information on patent ramily members

Inti onal Application No
PCT/IN2005/000037

Patent document cited in search report			Publication Pat date me		Patent family member(s)		Publication date
WO	2005057464	Α	23-06-2005	US	2005136480	A1	23-06-2005
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